

Appendix B**Primary Sequence Alignment of fabI protein from various pathogens.**

EC1259_FabI	1	-----	MGFLSGKRIIVTGVASKLSIAYGIAQS	27
HI1703_FabI	1	MRLVFLEILVGFVQRQIFAYTTQVFYANNIGKIMGFLTGKRIIVDGLASNRSIAYGIAKS	60	
PA1805_FabI	1	-----	MGFLTGKRIIVDGLASNRSIAYGIAKS	27
HP0195_FabI	1	-----	MGFLKGKKGLIVGVANNKSIAYGIAQS	27
EF0282_FabI	1	-----	MFLQNKNVVVMGVANKKSIAYGIAQS	26
SA2112_FabI	1	-----	MLNLENKTYVEMGIANKRSIAFGVAKV	27
EC1259_FabI	28	MHREGAELAFTYQNDKLEKGRVEEFAAQLGS--DIVLQCDVAEDASTDTMFAEELGKVWPKF	85	
HI1703_FabI	61	MKEOGAELAFTYLNNDKLQPRVEEFAKEFGS--DIVLPLDVATDESQNCFAEUSKRWDFK	118	
PA1805_FabI	28	MHREGAELAFTYQNDKLRGRVEEFASGWGSRPELCFPCDVADDQSIEAVFAALGKHWDFGL	87	
HP0195_FabI	28	CFNCGATLAFTYLNESLEKRVRPPIAQELNS--PYVYELDVSKEEHFKSLYNSVKKDLGSL	85	
EF0282_FabI	27	IKDQGANVINTYQNERMKKQVVKLADEND--LLIVECDVADASTQAAFETIKNEVGTI	82	
SA2112_FabI	28	LDQLGAKLWFTYRKERSRKETEKLLEQLNQPEAHLYQIDVQSDEEVINGFEQIGKDVGNI	87	
EC1259_FabI	86	DGFVHSIGFAPGDOI DGDYVNAVTREGFKTAHDISYSFVAMAKACRSMIN-PGSALLETL	144	
HI1703_FabI	119	DGFHIAIAFAPGDOI DGDYVNAATREGYRIAHDISYSFVAMQAARPYLN-PNAALLTL	177	
PA1805_FabI	88	DIIVHSVGFAPGDOI DGDFTAVTTRREGFRIAHDISYSFIAIAKAGREMMKGRNGSLLTL	147	
HP0195_FabI	86	DFTMHSVAFAPKEALEGSLLETS-KSAENTAMEISVSYLIEETNTLKPILN-NGASVETL	143	
EF0282_FabI	83	DGLVHIAIAFAKKKEELSGNVSDIT-REGFLLIAQDISYSSILIAVTHYAKPILN-PGSGIVTL	140	
SA2112_FabI	88	DGVYHSIAFANMEDURGRFSETS-REGFLLIAQDISYSLTIVAHHEAKKLMP-EGGSIVAT	145	
EC1259_FabI	145	SYLGAEERATIPNPNVNMGEAKASLEANVRYMANAMGPECVRVNAISAGPIRTLAAASGIKDFR	204	
HI1703_FabI	178	SYLGAEERATIPNPNVNMGEAKASLEANVATEVMAADLGKEIPRVNAISAGPIRTLAAASCIKNEK	237	
PA1805_FabI	148	SYLGAEERTMPNPNVNMGEAKASLEAGVRYLAGSLGAEGTRVNAISAGPIRTLAAASGIKSFR	207	
HP0195_FabI	144	SYLGSSTKYMAYHNVNMGEAKAALESAVRYLAVDLGKHHIRVNAISAGPIRTLASSGIADER	203	
EF0282_FabI	141	TYLGSEERATIPNPNVNMGEAKASLEATAVKYLAFELAADKIRVNGISAGAIKTLAVTGVKDYD	200	
SA2112_FabI	146	TYLGGEFAVQVNVNMGVAKASLEANVSKYLAIDLGPDNIRVNAISAGPIRTLSSAKGVGGFN	205	
EC1259_FabI	205	KMLAHCEAVTPIRRVTIEDVGNSAAEICSDLASAGISGEVWVHDGGESIAAMNELELK--	262	
HI1703_FabI	238	KMLSTFEKTAALRRVTIEDVGNSAAEICSDLASAGISGEVWVHDAGESITAMGELGEE--	295	
PA1805_FabI	208	KMLAANERQTPIERRVTIEEVGNAGAEICSDLASAGISGEVWVHDAGESITAMGPLDDD--	265	
HP0195_FabI	204	MILKWNNEINAPLRKNVSLEEVGNAGMYLLSSLSSGVSGEVWVFDAGYHVMGMGAVEEKDN	263	
EF0282_FabI	201	QIISISNERTPDXTGVTIEEVGNNTCAELVSDLASGVVGDITYVDKGVHLT-----	250	
SA2112_FabI	206	TNIKEIXERAPLKRNVDQVEVGKTAAYILSDLSSGVTGENIHVDSGFHAIK-----	256	
EC1259_FabI	262	-----	262	
HI1703_FabI	295	-----	295	
PA1805_FabI	265	-----	265	
HP0195_FabI	264	KATLLWDLHKEQ	275	
EF0282_FabI	250	-----	250	
SA2112_FabI	256	-----	256	